10/678,588

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CURRENT MACINTOSH VERSION IS V6.0c(ENG) AND V6.0Jc(JP),
AND CURRENT DISCOVER FILE IS DATED 13 JUNE 2005.
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=> file agricola caplus biosis

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=> s hap3
L1 190 HAP3

=> s l1 and (transgenic or tansform?)
L2 11 L1 AND (TRANSGENIC OR TANSFORM?)

=> d 1-11 ti

L2 ANSWER 1 OF 11 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2005) on STN
TI OsHAP3 genes regulate chloroplast biogenesis in rice.

L2 ANSWER 2 OF 11 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2005) on STN
TI LEAFY COTYLEDON1-LIKE defines a class of regulators essential for embryo development.

L2 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI Manipulating the oil composition of plants or seed by changing the balance between lipid and polysaccharide accumulation

L2 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant

L2 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI Plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants

L2 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI Use of corn, soybean or Arabidopsis transcription factor **Hap3** and Bacillus thuringiensis δ-endotoxin in improving tolerance of **transgenic** crops to water deficits, herbicide and insect resistance

L2 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI Rice LEC1 (leafy cotyledon 1 transcriptional activator) inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation

L2 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI OsHAP3 genes regulate chloroplast biogenesis in rice

L2 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI Alteration of oil traits in plants by transformation with cDNAs encoding associated proteins

L2 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
TI Transcriptional activator nucleic acids and polypeptides from plants

L2 ANSWER 11 OF 11 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
TI OsHAP3 genes regulate chloroplast biogenesis in rice.

=> d 1-11 all

L2 ANSWER 1 OF 11 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2005) on STN
AN 2004:4632 AGRICOLA
DN IND43612708

TI OsHAP3 genes regulate chloroplast biogenesis in rice.
AU Miyoshi, K.; Ito, Y.; Serizawa, A.; Kurata, N.
SO Plant journal, 2003 Nov. Vol. 36, no. 4 p. 532-540
ISSN: 0960-7412
NTE Includes references
DT Article
FS Non US
LA English
AB We have isolated three genes that potentially encode a **HAP3** /nuclear factor-YB (NF-YB)/CCAAT binding factor-A (CBF-A) subunit of a CCAAT-box binding complex in rice (Oryza sativa), and named them OsHAP3A, OsHAP3B and OsHAP3C. These genes were expressed in various organs including leaves. In the **transgenic** rice plants with antisense or RNAi construct of OsHAP3A, reduced expression of not only OsHAP3A but also OsHAP3B and OsHAP3C was observed. These plants had pale green leaves, in which the amount of chlorophyll was reduced and chloroplasts were degenerated. Lamella was not well developed and accumulation of starch was not detected. The degenerated chloroplast formation was accompanied by reduced expression of nuclear-encoded photosynthesis genes such as RBCS and CAB, while expression of chloroplast-encoded genes was not affected or rather increased. These results suggest that one or more OsHAP3 genes regulate the expression of nuclear-encoded chloroplast-targeted genes and normal development of chloroplasts.
CC F200 Plant Breeding and Genetics; F400 Plant Structure; F600 Plant Physiology and Biochemistry
CTLC DNA-binding proteins; Oryza sativa; amino acid sequences; antisense RNA; chloroplasts; gene expression; gene silencing; grain crops; leaves; nucleotide sequences; photosynthesis; plant anatomy; plant proteins; rice; rice protein; **transgenic** plants; ultrastructure
ST CBF-A protein; CCAAT binding factor; NF-YB protein; OsHAP3 gene; molecular sequence data; photosynthetic gene
RN 1406-65-1 (CHLOROPHYLL)
9005-25-8 (STARCH)
29091-21-2 (FACTOR)

L2 ANSWER 2 OF 11 AGRICOLA Compiled and distributed by the National Agricultural Library of the Department of Agriculture of the United States of America. It contains copyrighted materials. All rights reserved. (2005) on STN
AN 2003:17949 AGRICOLA
DN IND23314512
TI LEAFY COTYLEDON1-LIKE defines a class of regulators essential for embryo development.
AU Kwong, R.W.; Bui, A.Q.; Lee, H.; Kwong, L.W.; Fischer, R.L.; Goldberg, R.B.; Harada, J.J.
AV DNAL (QK725.P532)
SO The Plant cell, Jan 2003. Vol. 15, No. 1. p. 5-18
Publisher: [Rockville, MD : American Society of Plant Physiologists, c1989-
CODEN: PLCEEW; ISSN: 1040-4651
NTE Includes references
CY Maryland; United States
DT Article
FS U.S. Imprints not USDA, Experiment or Extension
LA English
AB Arabidopsis LEAFY COTYLEDON1 (LEC1) is a critical regulator required for normal development during the early and late phases of embryogenesis that is sufficient to induce embryonic development in vegetative cells. LEC1 encodes a **HAP3** subunit of the CCAAT binding transcription factor. We show that the 10 Arabidopsis **HAP3** (AHAP3) subunits can be divided into two classes based on sequence identity in their central, conserved B domain. LEC1 and its most closely related subunit, LEC1-LIKE (L1L), constitute LEC1-type AHAP3 subunits, whereas the remaining AHAP3 subunits are designated non-LEC1-type. Similar to LEC1, L1L is expressed primarily during seed development. However, suppression of L1L gene expression induced defects in embryo development that differed from those of lec1 mutants, suggesting that LEC1 and L1L play unique roles in embryogenesis. We show that L1L expressed under the control of DNA sequences flanking the LEC1 gene suppressed genetically the lec1 mutation,

suggesting that the LEC1-type B domains of L1L and LEC1 are critical for their function in embryogenesis. Our results also suggest that LEC1-type **HAP3** subunits arose from a common origin uniquely in plants. Thus, L1L, an essential regulator of embryo development, defines a unique class of plant **HAP3** subunits.

CC F200 Plant Breeding and Genetics; F600 Plant Physiology and Biochemistry

CT amino acid sequences; arabidopsis thaliana; complementary dna; embryonic development; fruits; gene expression; genetic regulation; messenger rna; nucleotide sequences; plant embryos; regulatory genes; seed development; transcription factors; **transgenic** plants

ST l1l gene; lec1 gene; molecular sequence data; rna interference; siliques

L2 ANSWER 3 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN

AN 2005:612464 CAPLUS

DN 143:130100

ED Entered STN: 15 Jul 2005

TI Manipulating the oil composition of plants or seed by changing the balance between lipid and polysaccharide accumulation

IN Singletary, George W.; Coaldrake, Peter; Krumpelman, Paulette M.; Nubel, Doug; Saunders, Court; Tarczynski, Mitchell C.; Zhou, Lan

PA Pioneer Hi-Bred International, Inc., USA; E. I. Du Pont de Nemours and Company

SO PCT Int. Appl., 174 pp.
CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-11
ICS C12N015-82; A01H005-00

CC 11-1 (Plant Biochemistry)
Section cross-reference(s): 3

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2005063988	A1	20050714	WO 2004-US43439	20041222
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IS, IT, LT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2005160494	A1	20050721	US 2004-21666	20041223
PRAI US 2003-532196P	P	20031223		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2005063988	ICM	C12N015-11
	ICS	C12N015-82; A01H005-00
WO 2005063988	ECLA	C12N015/82C4B2; C12N015/82C4B4
US 2005160494	NCL	800/281.000

AB Methods of increasing the oil content of seed by increasing the level of expression of genes associated with lipid biosynthesis and accumulation and lowering the level of expression of genes associated with polysaccharide, i.e. starch, accumulation are described. This is achieved by increasing the levels of expression of genes for transcriptional activators that increase lipid biosynthesis in a plant in combination with the inhibition or disruption of starch biosynthesis or starch storage, and optionally in combination with expression of another polynucleotide of interest. Gene expression may be inhibited in a number of ways, including the use of antisense or siRNAs and cosuppression. Compns. also include transformed plants, plant cells, plant tissues, and plant seeds comprising these nucleotide constructs. The methods and constructs find use in alteration of oil phenotype in a plant or plant part thereof. The use of the LEC1 transcription factor in combination with a cosuppressive allele of the AGP2 gene in corn is demonstrated. Progeny from a cross between a

homozygous LEC1 **transgenic** line and a line carrying the cosuppressive allele of the AGP2 gene segregated as expected. Seed from plants carrying both of these genes (either as heterozygotes or homozygotes) showed oil content up to 140% greater than that of controls.

ST plant seed oil compn lipid polysaccharide metab carbon flow; starch lipid metab carbon flow seed oil; corn LEC1 glucose phosphate adenylyltransferase sequence; fatty acid desaturase sequence corn

IT Gene, plant
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(AGP1, inhibition of expression of; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Gene, plant
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(AGP2, in manipulating plant carbohydrate metabolism; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Gene, plant
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(AGP2, inhibition of expression of; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Transcription factors
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(C/EBP (CCAAT box/enhancer element-binding protein), in manipulating plant lipid metabolism; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Transcription factors
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(HAP2 (heme-activated protein 2), in manipulating plant lipid metabolism; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Transcription factors
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(**HAP3**, in manipulating plant lipid metabolism; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Transcription factors
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(HAP5 (heme-activated protein 5), in manipulating plant lipid metabolism; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Transcription factors
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(LEC-1, increasing levels of; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Gene, plant
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(LEC1, in manipulating plant lipid metabolism; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Promoter (genetic element)
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(LTP2, expression of LEC1 gene from; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Promoter (genetic element)
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(OLE, expression of LEC1 gene from; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Lipids, biological studies
RL: AGR (Agricultural use); BSU (Biological study, unclassified); BIOL (Biological study); USES (Uses)
(biosynthesis of, altering carbon flow into; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT cDNA sequences
(for genes affecting carbohydrate and lipid metabolism of Zea mays;

manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Double stranded RNA
RNA
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(for inhibition of expression of AGP1 or AGP2 genes; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Seed
(manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Polysaccharides, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Arachis hypogaea
Arecaceae
Avena sativa
Brassica
Canola
Carthamus tinctorius
Cocos nucifera
Glycine max
Gossypium hirsutum
Helianthus annuus
Hordeum vulgare
Liliopsida
Linum usitatissimum
Magnoliopsida
Olea europaea
Oryza sativa
Panicum
Ricinus communis
Sorghum bicolor
Triticum aestivum
Zea mays
(manipulating seed composition in; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Protein sequences
(of proteins affecting carbohydrate and lipid metabolism of Zea mays; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Seed
(oilseed; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT RNA
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(short hairpin, for inhibition of expression of AGP1 or AGP2 genes; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT Fats and Glyceridic oils, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(vegetable; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT 858385-66-7 858385-68-9 858385-70-3 858385-72-5
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT 9005-25-8, Starch, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(biosynthesis of, limitation of; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT 9027-71-8
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene for, limiting expression of; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)

IT 9014-34-0
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)

(inhibition of; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)
IT 142097-19-6, GenBank M81603 158681-93-7, GenBank Z38111 273710-55-7, GenBank AF243045 335514-62-0, GenBank AY032604 344547-08-6, GenBank AF334959 384748-54-3, GenBank U71381 385653-56-5, GenBank AF134411 389202-75-9, GenBank L22344 390279-55-7, GenBank AF410176 426962-55-2, GenBank AY104549 426976-21-8, GenBank AY105915 482889-89-4, GenBank AAK95562
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)
IT 858385-65-6 858385-67-8 858385-69-0 858385-71-4 858385-73-6 858385-74-7 858385-75-8 858385-76-9
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)
IT 142805-58-1, MEK 172308-13-3
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(transcription activation via; manipulating oil composition of plants or seed by changing balance between lipid and polysaccharide accumulation)
IT 858387-22-1 858387-24-3 858387-26-5 858387-28-7
RL: PRP (Properties)
(unclaimed nucleotide sequence; manipulating the oil composition of plants or seed by changing the balance between lipid and polysaccharide accumulation)
IT 858387-23-2 858387-25-4 858387-27-6
RL: PRP (Properties)
(unclaimed protein sequence; manipulating the oil composition of plants or seed by changing the balance between lipid and polysaccharide accumulation)
RE.CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD
RE
(1) Doehlert, D; CROP SCIENCE 1991, V31(1), P151 CAPLUS
(2) E I Du Pont de Nemours And Company; WO 0200904 A 2002 CAPLUS
(3) E I Du Pont de Nemours And Company; WO 03001902 A 2003
(4) Martini; WO 9911805 A 1999 CAPLUS

L2 ANSWER 4 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2005:349060 CAPLUS
DN 142:405595
ED Entered STN: 22 Apr 2005
TI Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant
IN Heard, Jacqueline E.; Keddie, James S.; Creelman, Robert A.; Pineda, Omaira; Jiang, Cai-Zhong; Ratcliffe, Oliver; Kumimoto, Roderick W.; Gutterson, Neal I.; Sherman, Bradley K.
PA Mendel Biotechnology, Inc., USA
SO U.S. Pat. Appl. Publ., 137 pp., Cont.-in-part of U.S. Ser. No. 666,642.
CODEN: USXXCO
DT Patent
LA English
IC ICM A01H001-00
ICS C12N015-82; C12N015-29
INCL 800298000; 800278000; 536023600
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 11
FAN.CNT 68

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2005086718	A1	20050421	US 2003-675852	20030930
	EP 1566444	A2	20050824	EP 2005-7595	20001114
	EP 1566444	A3	20050831		
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI, CY, TR				
	AU 771024	B2	20040311	AU 2000-72261	20001214
	AU 771434	B2	20040325	AU 2000-72260	20001214
	US 2003188330	A1	20031002	US 2002-112887	20020318

	CA 2456979	AA	20030220	CA 2002-2456979	20020809
	US 2003217383	A1	20031120	US 2002-225068	20020809
	US 2005120408	A9	20050602		
	US 2003226173	A1	20031204	US 2002-225066	20020809
	US 2005160493	A9	20050721		
	EP 1485490	A2	20041215	EP 2002-757104	20020809
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	US 2003131386	A1	20030710	US 2002-278536	20021022
	US 2003093837	A1	20030515	US 2002-286264	20021101
	US 2004019927	A1	20040129	US 2003-374780	20030225
	US 2004045049	A1	20040304	US 2003-412699	20030410
	CA 2516645	AA	20040910	CA 2004-2516645	20040225
	WO 2004076638	A2	20040910	WO 2004-US5654	20040225
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI				
	RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2005172364	A1	20050804	US 2005-69255	20050228
PRAI	US 1999-125814P	P	19990323		
	US 1999-166228P	P	19991117		
	US 2000-533030	B2	20000322		
	US 2000-713994	B2	20001116		
	US 2001-837944	B2	20010418		
	US 2001-310847P	P	20010809		
	US 2001-336049P	P	20011119		
	US 2002-112887	A2	20020318		
	US 2002-171468	B2	20020614		
	US 2002-225066	A2	20020809		
	US 2002-225068	A2	20020809		
	US 2002-411837P	P	20020918		
	US 2002-286264	A2	20021101		
	US 2002-434166P	P	20021217		
	US 2003-374780	A2	20030225		
	US 2003-412699	A2	20030410		
	US 2003-666642	A2	20030918		
	AU 1998-62756	A3	19980206		
	US 1999-394519	B2	19990913		
	US 2000-489376	B2	20000121		
	US 2000-506720	B2	20000217		
	US 2000-532591	B3	20000322		
	US 2000-533029	A2	20000322		
	US 2000-533392	B2	20000322		
	US 2000-533648	B2	20000322		
	WO 2000-US9448	A2	20000406		
	US 2000-197899P	P	20000417		
	US 2000-227439P	P	20000822		
	EP 2000-980406	A3	20001114		
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	US 2002-225067	A2	20020809		
	WO 2002-US25805	W	20020809		
	US 2003-675852	A	20030930		
	WO 2004-US5654	W	20040225		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
US 2005086718	ICM	A01H001-00
	ICS	C12N015-82; C12N015-29
	INCL	800298000; 800278000; 536023600
US 2005086718	NCL	800/298.000
	ECLA	C07K014/415; C12N015/82A12; C12N015/82B; C12N015/82C4B4; C12N015/82C4B10; C12N015/82C8; C12N015/82C8A8; C12N015/82C8B; C12N015/82C8B2;

		C12N015/82C8B4A; C12N015/82C8B6B
US 20031.8.8330	NCL	800/278.000
	ECLA	C07K014/415; C12N015/82B; C12N015/82C4B4; C12N015/82C4B10; C12N015/82C8; C12N015/82C8A8; C12N015/82C8B2
US 2003217383	NCL	800/279.000
	ECLA	C07K014/415; C12N015/82C8; C12N015/82C8B; C12N015/82C8B2; C12N015/82C8B4A; C12N015/82C8B6B
US 2003226173	NCL	800/281.000
	ECLA	C07K014/415; C12N015/82C8; C12N015/82C8B; C12N015/82C8B2; C12N015/82C8B4A; C12N015/82C8B6B
US 2003131386	NCL	800/289.000
	ECLA	C07K014/415; C12N015/82C8
US 2003093837	NCL	800/287.000
	ECLA	C07K014/415; C12N015/82C8
US 2004019927	NCL	800/278.000
	ECLA	C07K014/415; C12N015/82C8B; C12N015/82C8; C12N015/82C8A8; C12N015/82C8B2
US 2004045049	NCL	800/278.000
	ECLA	C07K014/415; C12N015/82A12; C12N015/82C4B4; C12N015/82C8; C12N015/82C8A8; C12N015/82C8B; C12N015/82C8B2; C12N015/82C8B4A; C12N015/82C8B6B
WO 2004076638	ECLA	C07K014/415; C12N015/82C8B; C12N015/82C8B2
US 2005172364	NCL	800/289.000
	ECLA	C07K014/415; C12N015/82A12; C12N015/82B; C12N015/82C4B4; C12N015/82C4B10; C12N015/82C8; C12N015/82C8A8; C12N015/82C8B; C12N015/82C8B2; C12N015/82C8B6B

AB The invention relates to plant transcription factor polypeptides, polynucleotides that encode them, homologs from a variety of plant species, and methods of using the polynucleotides and polypeptides to produce **transgenic** plants having advantageous properties compared to a reference plant, including improved abiotic stress tolerance. Sequence information related to these polynucleotides and polypeptides can also be used in bioinformatic search methods to identify related sequences and is also disclosed. Specifically disclosed are protein and cDNA sequences of a CCAAT transcription factor G482 with the ability to regulate abiotic stress tolerance in a plant. G482 contains conserved CCAAT-box binding or B domain of **HAP3** subfamily transcription factors, with the motif of Asn-(Xaa)4-Lys-(Xaa)33-34-Asn-Gly. The G482 **transgenic** plant has increased tolerance to abiotic stress as compared to a nontransformed plant.

ST cDNA sequence plant **HAP3** transcription factor homolog G482 Arabidopsis; abiotic stress tolerance **transgenic** plant Arabidopsis G482 gene

IT Arabidopsis thaliana
Genetic engineering
Protein sequences
cDNA sequences
(Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Protein motifs
(B domain, G482 containing; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Gene, plant
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(G481; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Plant cell
(G482 transformation in; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Gene, plant
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(G482; Arabidopsis thaliana **HAP3** transcription factor homolog

G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Gene, plant
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(G485; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Transcription factors
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(**HAP3**, gene G481; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Transcription factors
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(**HAP3**, gene G482; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Transcription factors
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(**HAP3**, gene G485; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Cucumis melo
(cantaloupe, **transgenic**, expressing G482; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Brassica oleracea botrytis
(cauliflower, **transgenic**, expressing G482; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(constitutive, for **transgenic** G482 expressing; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Growth and development, plant
(flowering; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Genetic methods
(gene discovery; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Stress, plant
(heat, tolerance enhancement; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Germination
(in cold, tolerance enhancement; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(inducible, for **transgenic** G482 expressing; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Embryophyta
(lab cultivated, **transgenic**, expressing G482; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Evolution
(mol.; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic**

plant)
IT Stress, plant
(osmotic, tolerance enhancement; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)
IT Fruit
(rosaceous, **transgenic**, expressing G482; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)
IT Stress, plant
(salinity, tolerance enhancement; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)
IT Carbohydrates, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(sense alteration, by transfected G482; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)
IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(tissue-specific, for **transgenic** G482 expressing; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)
IT Allium cepa
Ananas comosus
Blackberry
Blueberry
Brassica
Brassica napus
Carica papaya
Citrullus lanatus
Citrus
Coffea
Cucumis sativus
Cucurbita
Cucurbita moschata
Cucurbita pepo
Daucus carota
Fragaria ananassa
Fruit tree
Glycine max
Gossypium hirsutum
Helianthus annuus
Lactuca sativa
Lycopersicon esculentum
Mangifera indica
Medicago sativa
Mint
Musa acuminata
Nicotiana tabacum
Oryza sativa
Piper
Pisum sativum
Raspberry
Saccharum officinarum
Solanum melongena
Solanum tuberosum
Spinacia oleracea
Trifolium
Triticum aestivum
Turf
Vitis vinifera
Zea mays
Zea mays saccharata
(**transgenic**, expressing G482; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)
IT Stress, plant

(water deficiency, tolerance enhancement; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT Stress, plant
(water deficiency; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT 850435-33-5 850435-35-7 850435-37-9
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT 850435-32-4 850435-34-6 850435-36-8
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; Arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT 850435-75-5 850435-77-7 850435-79-9 850435-81-3 850435-83-5
850435-85-7 850435-87-9 850435-89-1 850435-91-5 850435-93-7
850435-95-9 850436-01-0 850436-03-2 850436-05-4 850436-07-6
850436-09-8 850436-11-2 850436-13-4 850436-15-6 850436-17-8
850436-19-0 850436-21-4 850436-23-6 850436-25-8 850436-27-0
850436-29-2 850436-31-6 850436-33-8 850436-35-0 850436-37-2
850436-39-4 850436-41-8 850436-42-9 850436-44-1 850436-45-2
850436-47-4 850436-48-5 850436-50-9 850436-52-1 850436-53-2
850436-55-4 850436-57-6 850436-59-8 850436-61-2 850436-63-4
850436-65-6 850436-67-8 850436-68-9
RL: PRP (Properties)
(unclaimed nucleotide sequence; arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

IT 850435-76-6 850435-78-8 850435-80-2 850435-82-4 850435-84-6
850435-86-8 850435-88-0 850435-90-4 850435-92-6 850435-94-8
850435-96-0 850435-97-1 850435-98-2 850435-99-3 850436-00-9
850436-02-1 850436-04-3 850436-06-5 850436-08-7 850436-10-1
850436-12-3 850436-14-5 850436-16-7 850436-18-9 850436-20-3
850436-22-5 850436-24-7 850436-26-9 850436-28-1 850436-30-5
850436-32-7 850436-34-9 850436-36-1 850436-38-3 850436-40-7
850436-43-0 850436-46-3 850436-49-6 850436-51-0 850436-54-3
850436-56-5 850436-58-7 850436-60-1 850436-62-3 850436-64-5
850436-66-7
RL: PRP (Properties)
(unclaimed protein sequence; arabidopsis thaliana **HAP3** transcription factor homolog G482 regulating abiotic stress tolerance in a **transgenic** plant)

L2 ANSWER 5 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2005:324314 CAPLUS
DN 142:368725
ED Entered STN: 15 Apr 2005
TI Plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants
PA Monsanto Technology LLC, USA
SO PCT Int. Appl., 44 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12N015-82
CC 3-1 (Biochemical Genetics)
Section cross-reference(s): 11
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI WO 2005033319	A2	20050414	WO 2004-US32191	20041001
WO 2005033319	A3	20050825		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD,

GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC,
LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI,
NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY,
TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW
RW: BW, GH, GM, KE, LS, MW, MZ, NA, SD, SL, SZ, TZ, UG, ZM, ZW, AM,
AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK,
EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE,
SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE,
SN, TD, TG

PRAI US 2003-508409P P 20031002

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2005033319	ICM	C12N015-82
WO 2005033319	ECLA	C12N015/82C8; C12N015/82C8B2; C12N015/82C8B4; C12N015/82C8B4A; C12N015/82C8B4B; C12N015/82C8B6; C12N015/82C8B6E

AB The invention provides seeds for growing **transgenic** plants with a crop improvement trait by inserting into the genome of a progenitor plant a recombinant DNA construct which confers at least one crop improvement trait and, optionally, an herbicide resistance trait. Hybrid corn seed is produced by crossing a **transgenic** female ancestor corn plant having in its genome recombinant DNA which confers a crop improvement trait with a **transgenic** male ancestor corn plant having in its genome a recombinant DNA which confers at least one of an herbicide resistance trait of a pest resistance trait.

ST plant **Hap3** protein consensus sequence stacking crop improvement trait

IT Embryophyta
(C3-C4 intermediate plant; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Transcription factors
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(**HAP3**; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Gene, plant
RL: BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(**Hap3**; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Plant tissue
(abscission zone; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Embryophyta
(cold-tolerant plant; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Cell aging
(delay; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Leaf
(development; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Herbicides
(dinitroaniline, resistance to; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Growth and development, plant
(early maturity; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Seed
(endosperm; plant **Hap3** protein consensus sequence for

generating stacking crop improvement traits in **transgenic** plants)

IT Post-transcriptional processing
(gene silencing; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Hormones, plant
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(germination stimulators; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Herbicides
(imidazolinone, resistance to; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Stress, plant
(light, low light tolerance; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Seed
(oilseed; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Herbicides
(oxynil, resistance to; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Bacillus thuringiensis
Breeding, plant
Disease resistance, plant
Herbicide resistance
Insecticides
Molecular cloning
Photosynthesis, biological
Protein sequences
(plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Double stranded RNA
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Amino acids, preparation
Proteins
Vitamins
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Stem cell
(plant, **transgenic**; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Herbicides
(pyridine, resistance to; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Insecta
(resistance; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Herbicides
(sulfonamide, resistance to; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Herbicides
(sulfonylurea, resistance to; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Canola
Crop (plant)
Embryophyta
Glycine max
Gossypium hirsutum
Seed
Triticum aestivum
Zea mays
(**transgenic**; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Stress, plant
(water deficiency, tolerance; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT Toxins
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation); USES (Uses)
(δ-endotoxins; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT 849381-78-8P
RL: AGR (Agricultural use); BPN (Biosynthetic preparation); PRP (Properties); BIOL (Biological study); PREP (Preparation); USES (Uses)
(**Hap3** consensus sequence; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT 9005-25-8P, Starch, preparation
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT 7723-14-0, Phosphorus, biological studies 7727-37-9, Nitrogen, biological studies
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT 1071-83-6, Glyphosate 35597-43-4, Bialaphos 35597-44-5, Phosphinothricin 51276-47-2, Glufosinate
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(resistance to; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT 849386-57-8 849386-60-3 849386-61-4
RL: PRP (Properties)
(unclaimed nucleotide sequence; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

IT 849386-58-9 849386-59-0 849386-62-5 849386-63-6 849386-64-7 849386-65-8
RL: PRP (Properties)
(unclaimed protein sequence; plant **Hap3** protein consensus sequence for generating stacking crop improvement traits in **transgenic** plants)

L2 ANSWER 6 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2005:78323 CAPLUS
DN 142:173477
ED Entered STN: 28 Jan 2005
TI Use of corn, soybean or Arabidopsis transcription factor **Hap3** and Bacillus thuringiensis δ-endotoxin in improving tolerance of **transgenic** crops to water deficits, herbicide and insect resistance
IN Wu, Jingrui; Lee, Garrett J.; Adams, Thomas R.; Xie, Zhidong; Dotson, Stanton B.; Nelson, Donald E.
PA USA
SO U.S. Pat. Appl. Publ., 15 pp.
CODEN: USXXCO
DT Patent

LA English
IC ICM A01H001-00
ICS C12N015-82
INCL 800289000; 435468000
CC 11-5 (Plant Biochemistry)
Section cross-reference(s): 3, 6
FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	US 2005022266	A1	20050127	US 2003-678588	20031002
PRAI	US 2002-415758P	P	20021002		
	US 2002-425157P	P	20021108		
	US 2003-463787P	P	20030418		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
US 2005022266	ICM	A01H001-00
	ICS	C12N015-82
	INCL	800289000; 435468000
US 2005022266	NCL	800/289.000
	ECLA	C12N015/82C8B2

AB The present invention provides use of corn, soybean or Arabidopsis transcription factor **Hap3** and Bacillus thuringiensis δ-endotoxin in improving tolerance of **transgenic** crops to water deficits, herbicide and insect resistance. More specifically the DNA constructs comprise a polynucleotide which encodes at least a functional part of a transcription factor that is a CCAAT-box DNA binding subunit or a homologous transcription factor.

ST corn soybean Arabidopsis transcription factor **Hap3** sequence; Bacillus delta endotoxin **transgenic** crop herbicide insect resistance; drought tolerance delta endotoxin transcription factor **Hap3** plant transgene

IT Gene, plant
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(Ca-4H, water deficit-inducible promoter; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Transcription factors
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(**HAP3**; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Gene, plant
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(Hsp 17.5, water deficit-inducible promoter; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Gene, plant
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(Hva-22, water deficit-inducible promoter; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Gene, plant
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(Rab-17, water deficit-inducible promoter; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Herbicides
(dinitroaniline, resistance to; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Herbicides

(imidazolinone, resistance to; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Disease resistance, plant
(insect; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Herbicides
(oxynil, resistance to; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Herbicides
(pyridine, resistance to; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Herbicides
(sulfonamide, resistance to; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Herbicides
(sulfonylurea, resistance to; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Canola
Gossypium hirsutum
Oryza sativa
Poaceae
Seed
Triticum aestivum
(**transgenic**; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Arabidopsis thaliana
Bacillus thuringiensis
Crop (plant)
Glycine max
Herbicide resistance
Insecta
Plant pathogen
Protein sequences
Zea mays
(use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Stress, plant
(water deficiency, tolerance; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Promoter (genetic element)
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(water deficit-inducible; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT Toxins
RL: AGR (Agricultural use); BSU (Biological study, unclassified); BIOL (Biological study); USES (Uses)
(δ-endotoxins; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT 832266-03-2

RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(Transcription factor **Hap3** core domain consensus sequence; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT 832265-97-1, Transcription factor **Hap3** (Zea mays) 832265-98-2
832265-99-3, Transcription factor **Hap3** (Glycine max)
832266-00-9 832266-01-0 832266-02-1
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT 1071-83-6, Glyphosate 35597-43-4, Bialaphos 35597-44-5, Phosphinothricin 51276-47-2, Glufosinate
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(resistance to; use of transcription factor **Hap3** and Bacillus thuringiensis -endotoxin in improving tolerance of **transgenic** plants to water deficits, herbicide and insect resistance)

IT 832269-05-3 832269-06-4 832269-07-5
RL: PRP (Properties)
(unclaimed nucleotide sequence; use of corn, soybean or Arabidopsis transcription factor **Hap3** and Bacillus thuringiensis δ-endotoxin in improving tolerance of **transgenic** crops to water deficits, herbicide and insect resistance)

L2 ANSWER 7 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:60210 CAPLUS
DN 140:123711
ED Entered STN: 26 Jan 2004
TI Rice LEC1 (leafy cotyledon 1 transcriptional activator) inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation
IN Lowe, Keith S.; Gordon-Kamm, William J.
PA USA
SO U.S. Pat. Appl. Publ., 23 pp.
CODEN: USXXCO
DT Patent
LA English
IC ICM A01H001-00
ICS C12N015-82
INCL 800284000; 435468000
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 11
FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI US 2004016022	A1	20040122	US 2002-199609	20020719
PRAI US 2002-199609		20020719		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
US 2004016022	ICM	A01H001-00
	ICS	C12N015-82
	INCL	800284000; 435468000
US 2004016022	NCL	800/284.000
	ECLA	C07K014/415; C12N015/82C8D; C12N015/82C8

AB The invention provides novel uses for isolated LEC1 (leafy cotyledon 1 transcriptional activator), a known **HAP3** family member transcriptional activator polypeptide that regulates gene expression during embryo development. The invention further provides expression cassettes, transformed host cells, and **transgenic** plants and plant parts. In particular, rice LEC1 (leafy cotyledon 1 transcriptional activator), identified by sequence blasting of corn LEC1 in rice genomic database. As expected, ectopic expression of OsLEC1 induces somatic embryogenesis and induces apomixis in maize callus. Furthermore, OsLEC1 expression results in increased growth rates, which can be used as a

screening criterion for pos. selection of transformants. Indeed, re-transformation of OsLEC1 **transgenic** progeny results in increased transformation frequency in elite maize inbreds.
ST leafy cotyledon transcriptional activator LEC1 cDNA sequence rice; transformation selection enhancement LEC1 **transgenic** plant
IT Enzymes, biological studies
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(DNA-recombining, gene FLP, mediated LEC1 genomic integration; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Genetic element
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(FRT, LEC1 gene flanked by; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Transcription factors
RL: AGR (Agricultural use); REM (Removal or disposal); BIOL (Biological study); PROC (Process); USES (Uses)
(Polycomb, gene FIE (FERTILIZATION-INDEPENDENT ENDOSPERM), knockout plant to enhance transformation; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Reproduction, plant
(asexual, induction by LEC1; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Zea mays
(callus of; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Plant tissue
(callus, rice LEC1 transformation into; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT cDNA sequences
(for rice transcription activator LEC1; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Gene, plant
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(for rice transcription activator LEC1; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Genetic methods
(gene discovery; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Promoter (genetic element)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(in regulation of rice LEC1 expression; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Somatic embryogenesis, plant
(induction by LEC1; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Protein sequences
(of rice transcription activator LEC1; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Auxins
RL: ADV (Adverse effect, including toxicity); BIOL (Biological study)
(plant culture media containing; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Molecular cloning
Oryza sativa
(rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Transcription factors
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP

(Properties); BIOL (Biological study); USES (Uses)
(rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Transformation, genetic
(selection or enhancement using LEC1; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT RNA
RL: AGR (Agricultural use); BIOL (Biological study); USES (Uses)
(transformation into plant cells; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Canola
Glycine max
Gossypium hirsutum
Helianthus annuus
Liliopsida
Magnoliopsida
Medicago sativa
Oryza sativa
Plant cell
Plant tissue culture
Seed
Sorghum bicolor
Triticum aestivum
Zea mays
(transformation of; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Antisense DNA
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(transformation of; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT Embryophyta
(**transgenic**; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT 648630-22-2
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT 648630-21-1
RL: AGR (Agricultural use); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; rice LEC1 inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT 648630-67-5 648630-68-6
RL: PRP (Properties)
(unclaimed nucleotide sequence; rice LEC1 (leafy cotyledon 1 transcriptional activator) inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)
IT 648630-66-4
RL: PRP (Properties)
(unclaimed protein sequence; rice LEC1 (leafy cotyledon 1 transcriptional activator) inducing somatic embryogenesis and apomixis, methods of using it to enhance plant transformation)

L2 ANSWER 8 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2004:4865 CAPLUS
DN 140:194208
ED Entered STN: 05 Jan 2004
TI OsHAP3 genes regulate chloroplast biogenesis in rice
AU Miyoshi, Kazumaru; Ito, Yukihiro; Serizawa, Akiko; Kurata, Nori
CS Plant Genetics Laboratory, National Institute of Genetics, Mishima, Shizuoka-ken, 411-8540, Japan
SO Plant Journal (2003), 36(4), 532-540
CODEN: PLJUED; ISSN: 0960-7412
PB Blackwell Publishing Ltd.
DT Journal

LA English
CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 11
AB The authors have isolated three genes that potentially encode a **HAP3**/nuclear factor-YB (NF-YB)/CCAAT binding factor-A (CBF-A) subunit of a CCAAT-box binding complex in rice (Oryza sativa), and named them OsHAP3A, OsHAP3B and OsHAP3C. These genes were expressed in various organs including leaves. In the **transgenic** rice plants with antisense or RNAi construct of OsHAP3A, reduced expression of not only OsHAP3A but also OsHAP3B and OsHAP3C was observed These plants had pale green leaves, in which the amount of chlorophyll was reduced and chloroplasts were degenerated. Lamella was not well developed and accumulation of starch was not detected. The degenerated chloroplast formation was accompanied by reduced expression of nuclear-encoded photosynthesis genes such as RBCS and CAB, while expression of chloroplast-encoded genes was not affected or rather increased. These results suggest that one or more OsHAP3 genes regulate the expression of nuclear-encoded chloroplast-targeted genes and normal development of chloroplasts.
ST **HAP3** gene transcription factor chloroplast biogenesis rice sequence
IT Gene, plant
Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HAP3A; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Gene, plant
Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HAP3B; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Gene, plant
Transcription factors
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(HAP3C; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Transcriptional regulation
(activation; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Gene, plant
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(cab; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(chlorophyll a/b-binding, photosystem II, gene for; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Photosynthesis, biological
(genes for; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Gene, plant
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(rbcS; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT Chloroplast
Leaf
Oryza sativa japonica
Protein sequences

Root
cDNA sequences
(sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT 624628-21-3 624628-22-4 624628-23-5
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(amino acid sequence; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT 9027-23-0, Ribulose-1,5-bisphosphate carboxylase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene for; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
IT 513413-45-1, GenBank AB095438 513413-46-2, GenBank AB095439
513413-47-3, GenBank AB095440
RL: BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(nucleotide sequence; sequence of rice transcription factor **HAP3** genes and role in transcriptional regulation of photosynthesis-related genes and chloroplast biogenesis)
RE.CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD
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L2 ANSWER 9 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2003:23042 CAPLUS
DN 138:84476
ED Entered STN: 10 Jan 2003
TI Alteration of oil traits in plants by transformation with cDNAs encoding associated proteins
IN Allen, Stephen M.; Allen, William B.; Cahoon, Rebecca E.; Epelbaum, Sabine; Famodu, Omolayo O.; Harvell, Leslie T.; Jones, Todd J.; Kinney, Anthony J.; Klein, Theodore M.; Li, Changjiang; Oliveira, Igor Cunha; Sakai, Hajime; Shen, Bo; Tarczynski, Mitchell C.
PA E. I. Du Pont de Nemours & Co., USA; Pioneer Hi-Bred International, Inc.
SO PCT Int. Appl., 542 pp.
CODEN: PIXXD2
DT Patent
LA English
IC ICM C12Q
CC 3-2 (Biochemical Genetics)
Section cross-reference(s): 6, 11
FAN.CNT 1
PATENT NO. KIND DATE APPLICATION NO. DATE

PI	WO 2003002751	A2	20030109	WO 2002-US20152	20020627
	W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW				
	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2003126638	A1	20030703	US 2002-180375	20020626
	CA 2449238	AA	20030109	CA 2002-2449238	20020627
	CA 2449254	AA	20030109	CA 2002-2449254	20020627
	WO 2003001902	A2	20030109	WO 2002-US22086	20020627
	WO 2003001902	A3	20031016		
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	RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
	US 2003204870	A1	20031030	US 2002-183687	20020627
	EP 1412373	A2	20040428	EP 2002-749657	20020627
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	EP 1412375	A2	20040428	EP 2002-752280	20020627
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO, MK, CY, AL, TR				
	BR 2002011035	A	20040622	BR 2002-11035	20020627
PRAI	US 2001-301913P	P	20010629		
	WO 2002-US20152	W	20020627		
	WO 2002-US22086	W	20020627		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2003002751	ICM	C12Q
WO 2003002751	ECLA	C07K014/415; C12N015/82C4B4
US 2003126638	NCL	800/281.000
	ECLA	C07K014/415; C12N015/82C4B4
WO 2003001902	ECLA	C07K014/415; C12N015/82C4B4
US 2003204870	NCL	800/281.000
	ECLA	C07K014/415; C12N015/82C4B4
EP 1412373	ECLA	C07K014/415; C12N015/82C4B4

AB The preparation and use of nucleic acid fragments useful in altering the oil phenotype in plants are disclosed. Thus, cDNA clones encoding proteins involved in altering plant oil traits were identified by gene profiling and by conducting BLAST searches for similarity to sequences contained in the BLAST "nr" database. Proteins were identified with similarity to receptor protein kinases, MEK3 homologs, Hap2 homologs, LIP15 homologs, calcium EF-hand proteins, ATP citrate lyase, glucose metabolism proteins such as SNF1 homologs, Lec1 transcription factors, and seed developmentally regulated transcription factors such as CKC (Aintegumenta-like) homologs from various species including Arabidopsis thaliana, rice, corn, soybean, cucumber, Sordaria macrospora, sesame, grape, Brassica napus, and tobacco. Chimeric construct incorporating such nucleic acid fragments and suitable regulatory sequences can be used to create **transgenic** plants having altered lipid profiles. Methods for altering the oil phenotype in plants using such nucleic acid fragments also are disclosed.

ST oil phenotype plant transformation protein cDNA sequence

IT Transcription factors

RL: BSU (Biological study, unclassified); BIOL (Biological study) (AINTEGUMENTA, sequence homologs; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)

IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(CKC, sequence homologs; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HAP2 (heme-activated protein 2), sequence homologs; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(**HAP3**, sequence homologs; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(HAP5 (heme-activated protein 5), sequence homologs; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(LIP15 (low temperature-induced protein 15), sequence homologs; Alalteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Amaranthus retroflexus
Arabidopsis thaliana
Argemone mexicana
Brassica
Brassica napus
Breeding, plant
Canna edulis
Canola
Catalpa speciosa
Cocos nucifera
Cucumis sativus
Embryophyta
Eucalyptus tereticornis
Gene expression profiles, plant
Glycine max
Gossypium hirsutum
Helianthus annuus
Impatiens balsamina
Momordica charantia
Nicotiana benthamiana
Nicotiana tabacum
Oryza sativa
Seed
Sesamum indicum
Sordaria macrospora
Sorghum bicolor
Transformation, genetic
Triticum aestivum
Typha latifolia
Vernonia
Vitis vinifera
Zea mays
(alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Fats and Glyceridic oils, preparation
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Proteins
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(caleosin, sequence homologs; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Species differences
(genetic mapping of; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)

IT Genetic polymorphism
(mapping of; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT Genetic mapping
(of genetic variations; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT 482381-47-5 482381-49-7 482381-51-1 482381-53-3 482381-55-5
482381-57-7 482381-60-2 482381-62-4 482381-64-6 482381-66-8
482381-68-0 482381-70-4 482381-72-6 482381-74-8 482381-76-0
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482666-90-0 482666-92-2 482666-94-4 482666-96-6 482666-98-8
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RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(amino acid sequence; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)
IT 482381-46-4 482381-48-6 482381-50-0 482381-52-2 482381-54-4
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482667-20-9 482667-22-1
RL: BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); USES (Uses)
(nucleotide sequence; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)

IT 9027-95-6, ATP-citrate lyase 146702-84-3, MAP kinase kinase kinase 146838-21-3, Gene SNF1 protein kinase 347147-98-2, Receptor protein kinase 404344-49-6, MAPKKK3 kinase
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(sequence homologs; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)

IT 482676-09-5 482676-10-8 482676-11-9 482676-12-0 482676-13-1
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RL: PRP (Properties)
(unclaimed nucleotide sequence; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)

IT 482391-26-4 482391-27-5 482391-28-6 482391-29-7 482391-30-0
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482391-41-3 482391-42-4 482391-43-5 482391-44-6 482391-45-7
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482675-92-3 482675-93-4 482675-94-5 482675-95-6 482675-96-7
482675-97-8 482675-98-9 482675-99-0 482676-00-6 482676-01-7
482676-02-8 482676-03-9 482676-04-0 482676-05-1 482676-06-2
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482676-37-9
RL: PRP (Properties)
(unclaimed protein sequence; alteration of oil traits in plants by transformation with cDNAs encoding associated proteins)

L2 ANSWER 10 OF 11 CAPLUS COPYRIGHT 2005 ACS on STN
AN 2000:335579 CAPLUS
DN 133:1503
ED Entered STN: 19 May 2000
TI Transcriptional activator nucleic acids and polypeptides from plants
IN Lowe, Keith S.; Gordon-kamm, William J.; Klein, Theodore M.; Rasco-gaunt,

Sonriza; Cahoon, Rebecca E.; Sun, Xifan; Hoerster, George J.; Gregory, Carolyn Ann; Nadimpalli, Ramgopal

PA. Pioneer Hi-Bred International, Inc., USA; E. I. Du Pont de Nemours & Co.

SO PCT Int. Appl., 94 pp.
CODEN: PIXXD2

DT Patent

LA English

IC ICM C12N015-82
ICS C07K014-415; C12N015-11; A01H005-00

CC 3-3 (Biochemical Genetics)
Section cross-reference(s): 6, 11

FAN.CNT 1

	PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
PI	WO 2000028058	A2	20000518	WO 1999-US26514	19991109
	WO 2000028058	A3	20001012		
	W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
	RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG				
	US 6825397	B1	20041130	US 1999-435054	19991108
	CA 2348240	AA	20000518	CA 1999-2348240	19991109
	EP 1131454	A2	20010912	EP 1999-971859	19991109
	R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO				
	JP 2002529096	T2	20020910	JP 2000-581224	19991109
	AU 768243	B2	20031204	AU 2000-14741	19991109
	US 2004168217	A1	20040826	US 2003-744149	20031222
	US 2005034193	A1	20050210	US 2003-744620	20031222
PRAI	US 1998-107643P	P	19981109		
	US 1998-107810P	P	19981110		
	US 1999-435054	A3	19991108		
	WO 1999-US26514	W	19991109		

CLASS

PATENT NO.	CLASS	PATENT FAMILY CLASSIFICATION CODES
WO 2000028058	ICM	C12N015-82
	ICS	C07K014-415; C12N015-11; A01H005-00
WO 2000028058	ECLA	C07K014/415; C12N015/82C8; C12N015/82A8; C12N015/82C8D
US 6825397	NCL	800/278.000; 536/023.600; 536/024.100; 536/024.500; 800/286.000; 800/287.000; 800/295.000; 800/298.000; 800/306.000; 800/312.000; 800/316.000; 800/320.000; 800/320.100; 800/320.200; 800/320.300; 800/322.000
	ECLA	C07K014/415; C12N015/82A8; C12N015/82C8; C12N015/82C8D
US 2004168217	NCL	800/288.000
	ECLA	C07K014/415; C12N015/82A8; C12N015/82C8; C12N015/82C8D
US 2005034193	NCL	800/298.000
	ECLA	C07K014/415; C12N015/82A8; C12N015/82C8; C12N015/82C8D

AB The invention provides isolated nucleic acids and their encoded proteins which act as transcriptional activators and methods of use thereof. The transcriptional activators (designated LEC1 or leafy cotyledon 1) are homologous to other plant **Hap3**-type ccaat-box transcriptional activators, and were detected from cDNA libraries from corn, poppy (Argemone mexicana), soybean, Veronica melissaefolia, and wheat. The invention further provides expression cassettes, transformed host cells, **transgenic** plants and plant parts, and antibody compns. These transcriptional activators are found to improve the transformation frequency in plant tissue cultures, induce somatic embryogenesis and apomixis, suppress FIE polycomb expression, and increase the recovery of regenerated plants from culture systems.

ST transcription activator LEC1 cDNA sequence plant; transformation transcription activator LEC1 plant; regeneration transcription activator LEC1 plant; apomixis transcription activator LEC1 plant; somatic embryogenesis transcription activator LEC1 plant

IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(C/EBP (CCAAT box/enhancer element-binding protein), homologs;
transcriptional activator nucleic acids and polypeptides from plants)
IT Transcription factors
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(LEC1 (leafy cotyledon 1); transcriptional activator nucleic acids and polypeptides from plants)
IT Protein motifs
(LEC1 consensus domain; transcriptional activator nucleic acids and polypeptides from plants)
IT Growth and development, plant
(apomixis, induction of; transcriptional activator nucleic acids and polypeptides from plants)
IT DNA repair
(excision, improved efficiency of FLP-mediated; transcriptional activator nucleic acids and polypeptides from plants)
IT cDNA sequences
(for transcriptional activator from plants)
IT Transcription factors
RL: BSU (Biological study, unclassified); BIOL (Biological study)
(gene **HAP3**, homologs; transcriptional activator nucleic acids and polypeptides from plants)
IT Transcription factors
RL: BPR (Biological process); BSU (Biological study, unclassified); BIOL (Biological study); PROC (Process)
(gene Polycomb, suppression of expression of; transcriptional activator nucleic acids and polypeptides from plants)
IT Regeneration, plant
Somatic embryogenesis, plant
Transformation, genetic
(improved efficiency of; transcriptional activator nucleic acids and polypeptides from plants)
IT Animal tissue culture
(improved transformation efficiency and regeneration and somatic embryogenesis by; transcriptional activator nucleic acids and polypeptides from plants)
IT Reproduction, plant
(male sterility; transcriptional activator nucleic acids and polypeptides from plants)
IT Protein sequences
(of transcriptional activator from plants)
IT Alfalfa (Medicago sativa)
Argemone
Argemone mexicana
Canola
Corn
Cotton
Molecular cloning
Plant (Embryophyta)
Rice (Oryza sativa)
Sorghum
Soybean (Glycine max)
Sunflower
Veronica
Veronica melissaefolia
Wheat
(transcriptional activator nucleic acids and polypeptides from plants)
IT Primers (nucleic acid)
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(transcriptional activator nucleic acids and polypeptides from plants)
IT Plant cell
Seed
(**transgenic**; transcriptional activator nucleic acids and polypeptides from plants)

IT 269659-96-3 269659-97-4 269659-99-6 269660-01-7 269660-03-9
269660-05-1 269660-07-3 269660-09-5 269660-11-9 269734-02-3
RL: BAC (Biological activity or effector, except adverse); BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(amino acid sequence; transcriptional activator nucleic acids and polypeptides from plants)
IT 269659-90-7 269659-95-2 269659-98-5 269660-00-6 269660-02-8
269660-04-0 269660-06-2 269660-08-4 269660-10-8
RL: BOC (Biological occurrence); BSU (Biological study, unclassified); BUU (Biological use, unclassified); PRP (Properties); BIOL (Biological study); OCCU (Occurrence); USES (Uses)
(nucleotide sequence; transcriptional activator nucleic acids and polypeptides from plants)
IT 269659-92-9 269659-93-0 269659-94-1
RL: BUU (Biological use, unclassified); BIOL (Biological study); USES (Uses)
(primer; transcriptional activator nucleic acids and polypeptides from plants)
IT 250352-89-7 269660-40-4, 27: PN: WO0028058 PAGE: 59 unclaimed DNA
269660-41-5, 28: PN: WO0028058 PAGE: 59 unclaimed DNA
RL: PRP (Properties)
(unclaimed nucleotide sequence; transcriptional activator nucleic acids and polypeptides from plants)
IT 269660-42-6 269660-43-7 269660-44-8 269660-45-9 269660-46-0
269660-47-1 269660-48-2 269660-49-3 269733-86-0
RL: PRP (Properties)
(unclaimed protein sequence; transcriptional activator nucleic acids and polypeptides from plants)

L2 ANSWER 11 OF 11 BIOSIS COPYRIGHT (c) 2005 The Thomson Corporation on STN
AN 2004:21612 BIOSIS
DN PREV200400009515
TI OsHAP3 genes regulate chloroplast biogenesis in rice.
AU Miyoshi, Kazumaru; Ito, Yukihiro; Serizawa, Akiko; Kurata, Nori [Reprint Author]
CS Plant Genetics Laboratory, National Institute of Genetics, 1111 Yata, Mishima, Shizuoka-ken, 411-8540, Japan
nkurata@lab.nig.ac.jp
SO Plant Journal, (November 2003) Vol. 36, No. 4, pp. 532-540. print.
ISSN: 0960-7412 (ISSN print).
DT Article
LA English
OS DDBJ-AB095438; EMBL-AB095438; GenBank-AB095438; DDBJ-AB095439; EMBL-AB095439; GenBank-AB095439; DDBJ-AB095440; EMBL-AB095440; GenBank-AB095440
ED Entered STN: 24 Dec 2003
Last Updated on STN: 24 Dec 2003
AB We have isolated three genes that potentially encode a **HAP3** /nuclear factor-YB (NF-YB)/CCAAT binding factor-A (CBF-A) subunit of a CCAAT-box binding complex in rice (Oryza sativa), and named them OsHAP3A, OsHAP3B and OsHAP3C. These genes were expressed in various organs including leaves. In the **transgenic** rice plants with antisense or RNAi construct of OsHAP3A, reduced expression of not only OsHAP3A but also OsHAP3B and OsHAP3C was observed. These plants had pale green leaves, in which the amount of chlorophyll was reduced and chloroplasts were degenerated. Lamella was not well developed and accumulation of starch was not detected. The degenerated chloroplast formation was accompanied by reduced expression of nuclear-encoded photosynthesis genes such as RBCS and CAB, while expression of chloroplast-encoded genes was not affected or rather increased. These results suggest that one or more OsHAP3 genes regulate the expression of nuclear-encoded chloroplast-targeted genes and normal development of chloroplasts.
CC Cytology - General 02502
Cytology - Plant 02504
Genetics - General 03502
Genetics - Plant 03504

Biochemistry studies - Nucleic acids, purines and pyrimidines 10062
Biochemistry studies - Proteins, peptides and amino acids 10064
Development and Embryology - General and descriptive 25502
Plant physiology - Growth, differentiation 51510

IT Major Concepts
Cell Biology; Development; Molecular Genetics (Biochemistry and Molecular Biophysics)

IT Parts, Structures, & Systems of Organisms
chloroplast, biogenesis; leaf

IT Chemicals & Biochemicals
CCAAT-box binding complex; chlorophyll

IT Sequence Data
AB095438: DDBJ, EMBL, GenBank, amino acid sequence, nucleotide sequence; AB095439: DDBJ, EMBL, GenBank, amino acid sequence, nucleotide sequence; AB095440: DDBJ, EMBL, GenBank, amino acid sequence, nucleotide sequence

ORGN Classifier
Gramineae 25305

Super Taxa
Monocotyledones; Angiospermae; Spermatophyta; Plantae

Organism Name
Oryza sativa (species) [rice (common)]

Taxa Notes
Angiosperms, Monocots, Plants, Spermatophytes, Vascular Plants

GEN Oryza sativa CAB gene (Gramineae); Oryza sativa OsHAP3A gene (Gramineae): chloroplast biogenesis regulation; Oryza sativa OsHAP3B gene (Gramineae): chloroplast biogenesis regulation; Oryza sativa OsHAP3C gene (Gramineae): chloroplast biogenesis regulation; Oryza sativa RBCS gene (Gramineae)